

# SEQUENCE LISTING

<110> Teijin Pharma Limited

<120> New Secretory Protein

<130> SAP-715-PCT

<160> 9

<170> PatentIn version 3.1

<210> 1

<211> 978

<212> DNA

<213> human

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<221> CDS

<222> (1)..(951)

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Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Asp Cys His Ile Leu Asn

1 5 10 15

gca gaa gct ttt aaa tcc aag aaa ata tgt aaa tca ctt aag att tgt 96

Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys Ile Cys

20 25 30

gga ctg gtg ttt ggt atc ctg gcc cta act cta att gtc ctg ttt tgg 144

Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	Leu	Phe	Trp	
		35				40						45				
ggg	agc	aag	cac	ttc	tgg	ccg	gag	gta	ccc	aaa	aaa	gcc	tat	gac	atg	192
Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	Ala	Tyr	Asp	Met	
		50				55						60				
gag	cac	act	ttc	tac	agc	aat	gga	gag	aag	aag	aag	att	tac	atg	gaa	240
Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	Lys	Ile	Tyr	Met	Glu	
		65				70						75			80	
att	gat	cct	gtg	acc	aga	act	gaa	ata	ttc	aga	agc	gga	aat	ggc	act	288
Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	Arg	Ser	Gly	Asn	Gly	Thr	
				85					90					95		
gat	gaa	aca	ttg	gaa	gta	cac	gac	ttt	aaa	aac	gga	tac	act	ggc	atc	336
Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	Lys	Asn	Gly	Tyr	Thr	Gly	Ile	
		100							105					110		
tac	ttc	gtg	ggt	ctt	caa	aaa	tgt	ttt	atc	aaa	act	cag	att	aaa	gtg	384
Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	
		115							120					125		
att	cct	gaa	ttt	tct	gaa	cca	gaa	gag	gaa	ata	gat	gag	aat	gaa	gaa	432
Ile	Pro	Glu	Phe	Ser	Glu	Pro	Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	
		130							135					140		
att	acc	aca	act	ttc	ttt	gaa	cag	tca	gtg	att	tgg	gtc	cca	gca	gaa	480
Ile	Thr	Thr	Thr	Phe	Phe	Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	

145	150	155	160	
aag cct att gaa aac cga gat ttt ctt aaa aat tcc aaa att ctg gag				528
Lys Pro Ile Glu Asn Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu				
	165	170	175	
att tgt gat aac gtg acc atg tat tgg atc aat ccc act cta ata tca				576
Ile Cys Asp Asn Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ser				
	180	185	190	
gtt tct gag tta caa gac ttt gag gag gag gga gaa gat ctt cac ttt				624
Val Ser Glu Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu His Phe				
	195	200	205	
cct gcc aac gaa aaa aaa ggg att gaa caa aat gaa cag tgg gtg gtc				672
Pro Ala Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val				
	210	215	220	
cct caa gtg aaa gta gag aag acc cgt cac gcc aga caa gca agt gag				720
Pro Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu				
225	230	235	240	
gaa gaa ctt cca ata aat gac tat act gaa aat gga ata gaa ttt gat				768
Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe Asp				
	245	250	255	
ccc atg ctg gat gag aga ggt tat tgt tgt att tac tgc cgt cga ggc				816
Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg Arg Gly				
	260	265	270	

aac cgc tat tgc cgc cgc gtc tgt gaa cct tta cta ggc tac tac cca 864  
 Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly Tyr Tyr Pro  
 275 280 285

tat cca tac tgc tac caa gga gga cga gtc atc tgt cgt gtc atc atg 912  
 Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys Arg Val Ile Met  
 290 295 300

cct tgt aac tgg tgg gtg gcc cgc atg ctg ggg agg gtc gactacaaag 961  
 Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg Val  
 305 310 315

acgatgacga caagtga 978

<210> 2

<211> 317

<212> PRT

<213> human

<400> 2

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Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys Ile Cys  
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Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val Leu Phe Trp

35

40

45

Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys Ala Tyr Asp Met

50

55

60

Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys Lys Ile Tyr Met Glu

65

70

75

80

Ile Asp Pro Val Thr Arg Thr Glu Ile Phe Arg Ser Gly Asn Gly Thr

85

90

95

Asp Glu Thr Leu Glu Val His Asp Phe Lys Asn Gly Tyr Thr Gly Ile

100

105

110

Tyr Phe Val Gly Leu Gln Lys Cys Phe Ile Lys Thr Gln Ile Lys Val

115

120

125

Ile Pro Glu Phe Ser Glu Pro Glu Glu Glu Ile Asp Glu Asn Glu Glu

130

135

140

Ile Thr Thr Thr Phe Phe Glu Gln Ser Val Ile Trp Val Pro Ala Glu

145

150

155

160

Lys Pro Ile Glu Asn Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu

165

170

175

Ile Cys Asp Asn Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ser

180

185

190

Val Ser Glu Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu His Phe  
195 200 205

Pro Ala Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val  
210 215 220

Pro Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu  
225 230 235 240

Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe Asp  
245 250 255

Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg Arg Gly  
260 265 270

Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly Tyr Tyr Pro  
275 280 285

Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys Arg Val Ile Met  
290 295 300

Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg Val  
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<210> 3

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<212> DNA

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<221> CDS

<222> (1).. (246)

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1 5 10 15

ata gaa ttt gat ccc atg ctg gat gag aga ggt tat tgt tgt att tac 96

Ile Glu Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr

20 25 30

tgc cgt cga ggc aac cgc tat tgc cgc cgc gtc tgt gaa cct tta cta 144

Cys Arg Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu

35 40 45

ggc tac tac cca tat cca tac tgc tac caa gga gga cga gtc atc tgt 192

Gly Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys

50 55 60

cgt gtc atc atg cct tgt aac tgg tgg gtg gcc cgc atg ctg ggg agg 240

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg

65 70 75 80

gtc taa 246

Val

<210> 4

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Ile Glu Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr

20 25 30

Cys Arg Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu

35 40 45

Gly Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys

50 55 60

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg

65 70 75 80

Val



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<400> 5

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aag tcg cga caa gca agt gag gaa gaa ctt cca ata aat gac tat act	96
Lys Ser Arg Gln Ala Ser Glu Glu Glu Leu Pro Ile Asn Asp Tyr Thr	
20                      25                      30	

gaa aat gga ata gaa ttt gat ccc atg ctg gat gag aga ggt tat tgt	144
Glu Asn Gly Ile Glu Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys	
35                      40                      45	

tgt att tac tgc cgt cga ggc aac cgc tat tgc cgc cgc gtc tgt gaa	192
Cys Ile Tyr Cys Arg Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu	
50                      55                      60	

cct tta cta ggc tac tac cca tat cca tac tgc tac caa gga gga cga	240
Pro Leu Leu Gly Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg	

65	70	75	80	
gtc atc tgt cgt gtc atc atg cct tgt aac tgg tgg gtg gcc cgc atg				288
Val Ile Cys Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met				
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ctg ggg agg gtc taa	303
Leu Gly Arg Val	
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<210> 6

<211> 100

<212> PRT

<213> human

  

<400> 6

Met His His His His His His Asp Ile Asp Tyr Lys Asp Asp Asp Asp
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Lys Ser Arg Gln Ala Ser Glu Glu Glu Leu Pro Ile Asn Asp Tyr Thr
20                      25                      30

Glu Asn Gly Ile Glu Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys
35                      40                      45

Cys Ile Tyr Cys Arg Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu
50                      55                      60

Pro Leu Leu Gly Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg  
65 70 75 80

Val Ile Cys Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met  
85 90 95

Leu Gly Arg Val  
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<212> DNA

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<222> (1).. (420)

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1 5 10 15

aag tcg cga gaa gtg gta aga aaa att gtt cca act acc aca aaa aga 96  
Lys Ser Arg Glu Val Val Arg Lys Ile Val Pro Thr Thr Thr Lys Arg  
20 25 30

cca cac agt gga cca cgg agc aac cca ggc gct gga aga ctg aat aat	144
Pro His Ser Gly Pro Arg Ser Asn Pro Gly Ala Gly Arg Leu Asn Asn	
35 40 45	
 gaa acc aga ccc agt gtt caa gag gac tca caa gcc ttc aat cct gat	192
Glu Thr Arg Pro Ser Val Gln Glu Asp Ser Gln Ala Phe Asn Pro Asp	
50 55 60	
 aat cct tat cat cag cag gaa ggg gaa agc atg aca ttc gac cct aga	240
Asn Pro Tyr His Gln Gln Glu Gly Glu Ser Met Thr Phe Asp Pro Arg	
65 70 75 80	
 ctg gat cac gaa gga atc tgt tgt ata gaa tgt agg cgg agc tac acc	288
Leu Asp His Glu Gly Ile Cys Cys Ile Glu Cys Arg Arg Ser Tyr Thr	
85 90 95	
 cac tgc cag aag atc tgt gaa ccc ctg ggg ggc tat tac cca tgg cct	336
His Cys Gln Lys Ile Cys Glu Pro Leu Gly Gly Tyr Tyr Pro Trp Pro	
100 105 110	
 tat aat tat caa ggc tgc cgt tgc gcc tgc aga gtc atc atg cca tgt	384
Tyr Asn Tyr Gln Gly Cys Arg Ser Ala Cys Arg Val Ile Met Pro Cys	
115 120 125	
 agc tgg tgg gtg gcc cgt atc ttg ggc atg gtg tga	420
Ser Trp Trp Val Ala Arg Ile Leu Gly Met Val	
130 135	

<210> 8

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<212> PRT

<213> human

<400> 8

Met His His His His His His Asp Ile Asp Tyr Lys Asp Asp Asp Asp

1 5 10 15

Lys Ser Arg Glu Val Val Arg Lys Ile Val Pro Thr Thr Thr Lys Arg

20 25 30

Pro His Ser Gly Pro Arg Ser Asn Pro Gly Ala Gly Arg Leu Asn Asn

35 40 45

Glu Thr Arg Pro Ser Val Gln Glu Asp Ser Gln Ala Phe Asn Pro Asp

50 55 60

Asn Pro Tyr His Gln Gln Glu Gly Glu Ser Met Thr Phe Asp Pro Arg

65 70 75 80

Leu Asp His Glu Gly Ile Cys Cys Ile Glu Cys Arg Arg Ser Tyr Thr

85 90 95

His Cys Gln Lys Ile Cys Glu Pro Leu Gly Gly Tyr Tyr Pro Trp Pro

100 105 110

Tyr Asn Tyr Gln Gly Cys Arg Ser Ala Cys Arg Val Ile Met Pro Cys

115

120

125

Ser Trp Trp Val Ala Arg Ile Leu Gly Met Val

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135

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<212> PRT

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10

15

Glu Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys

20

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30

Arg Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly

35

40

45

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys Arg

50

55

60

Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg Val

65

70

75

80